

## FIG. 1

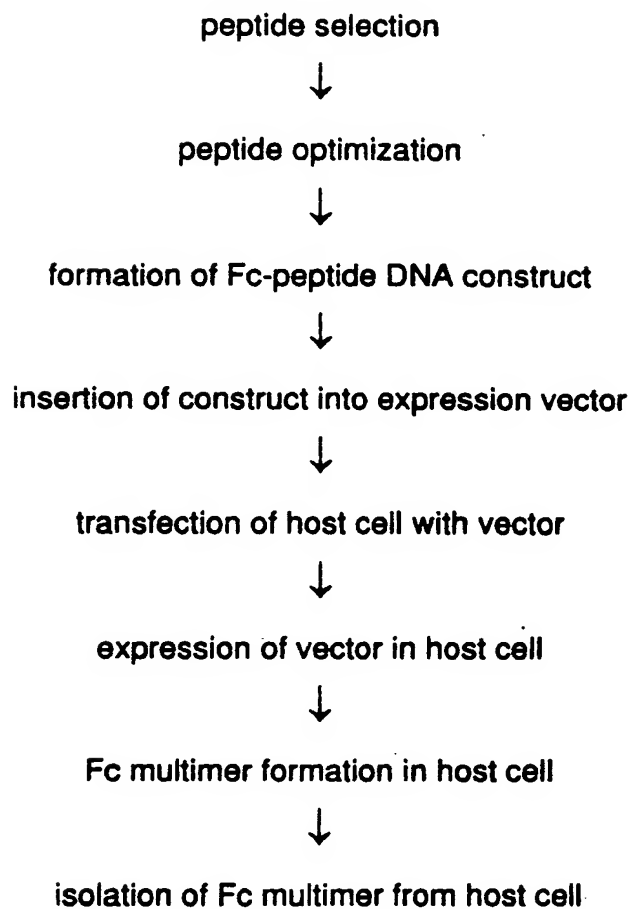


FIG. 2A

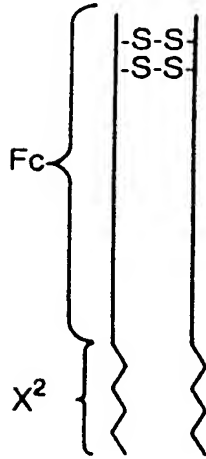


FIG. 2B

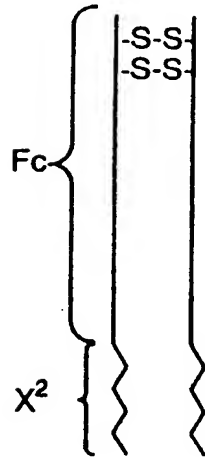


FIG. 2C

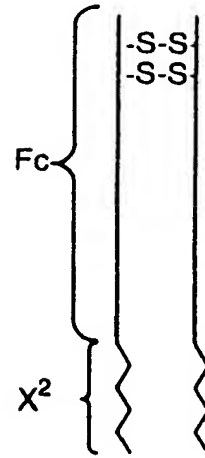


FIG. 2D

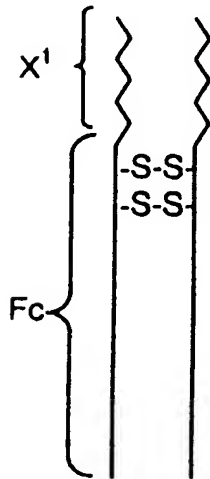


FIG. 2E

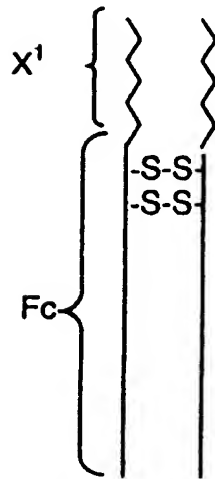


FIG. 2F

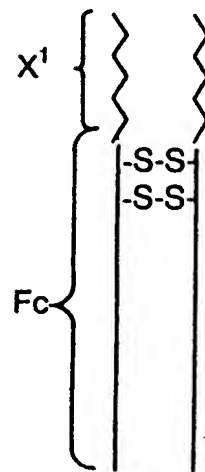


FIG. 3A



FIG. 3B

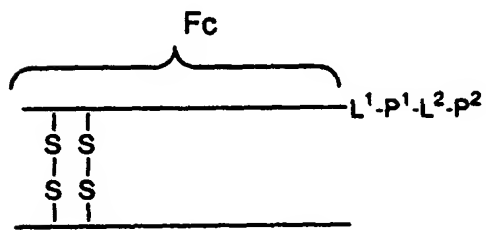
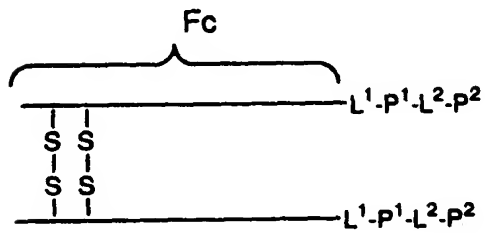


FIG. 3C



# FIG. 4

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ATGGACAAACTCACACATGTCCACCTTGTCAGCTCCGGAACCTCTGGGGGGACCGTCA
1  -----+-----+-----+-----+-----+-----+-----+-----+ 60
TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT

a      M D K T H T C P P C P A P E L L G G P S -

GTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
61  -----+-----+-----+-----+-----+-----+-----+-----+ 120
CAGAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG

a      V F L F P P K P K D T L M I S R T P E V -

ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a      T C V V V D V S H E D P E V K F N W Y V -

GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
CTGCCGCACCTCCACGTATTACGGTTCCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC

a      D G V E V H N A K T K P R E E Q Y N S T -

TACCGTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTTGACCGACTTACCGTTCCTCATG

a      Y R V V S V L T V L H Q D W L N G K E Y -

AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
TTCACGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG

a      K C K V S N K A L P A P I E K T I S K A -

AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG

a      K G Q P R E P Q V Y T L P P S R D E L T -

AAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a      K N Q V S L T C L V K G F Y P S D I A V -

GAGTGGGAGAGCAATGGGCAGCCGAGAACAACACAAGACCACGCCCTCCCGTGTCTGGAC
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
CTCACCCCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGACCTG

a      E W E S N G Q P E N N Y K T T P P V L D -

TCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAG
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC

a      S D G S F F L Y S K L T V D K S R W Q Q -

GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
CCCTTGCAGAAGAGTACGAGGCACCTACGTACTCCGAGACGTGTTGGTGTATGTGCGTCTTC

a      G N V F S C S V M H E A L H N H Y T Q K -

AGCCTCTCCCTGTCTCCGGGTAAA
661 -----+-----+-----+-----+-----+-----+-----+-----+ 684
TCGGAGAGGGACAGAGGCCCATTT

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FIG. 5

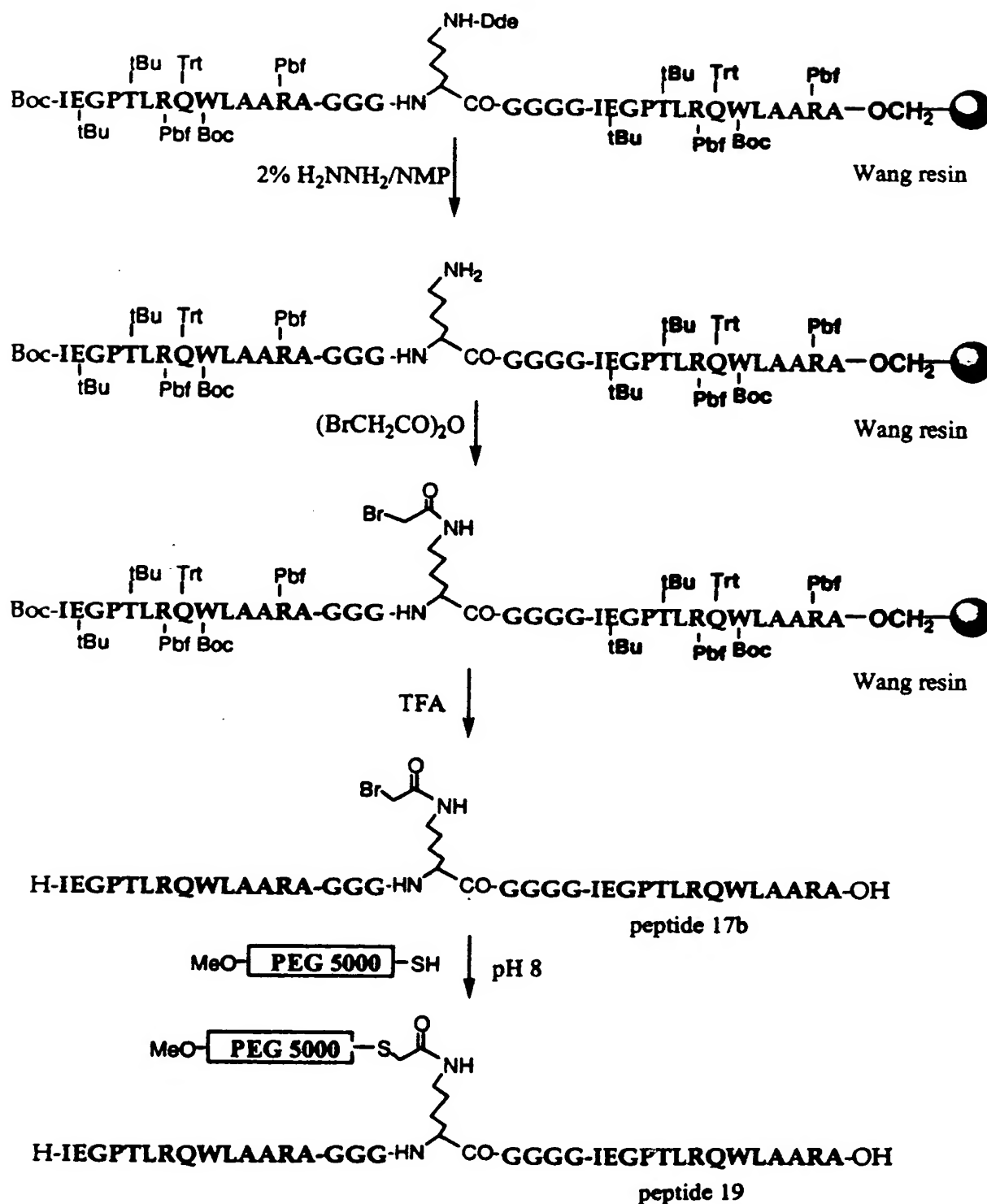
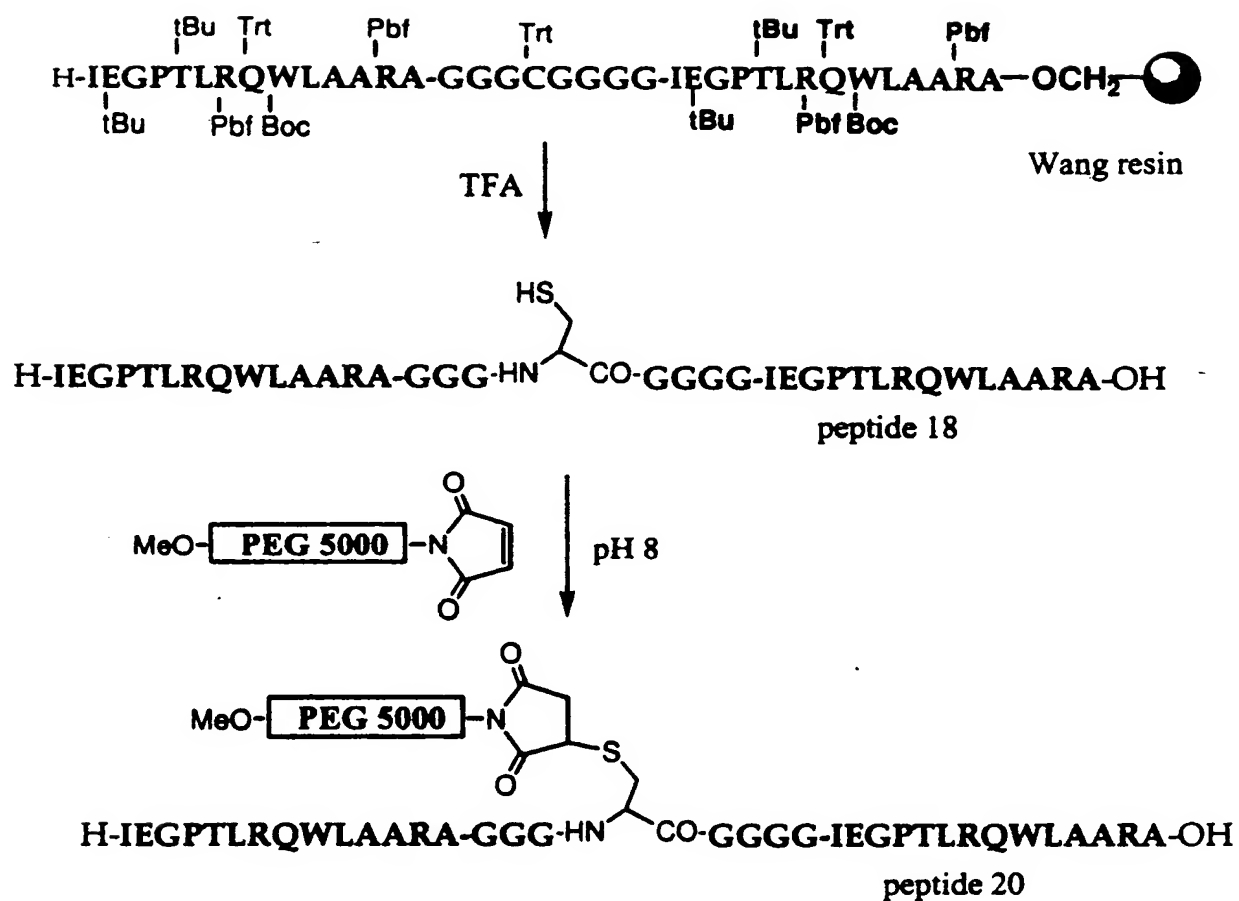


FIG. 6



[illegible]

FIG. 8

[illegible]







FIG.11

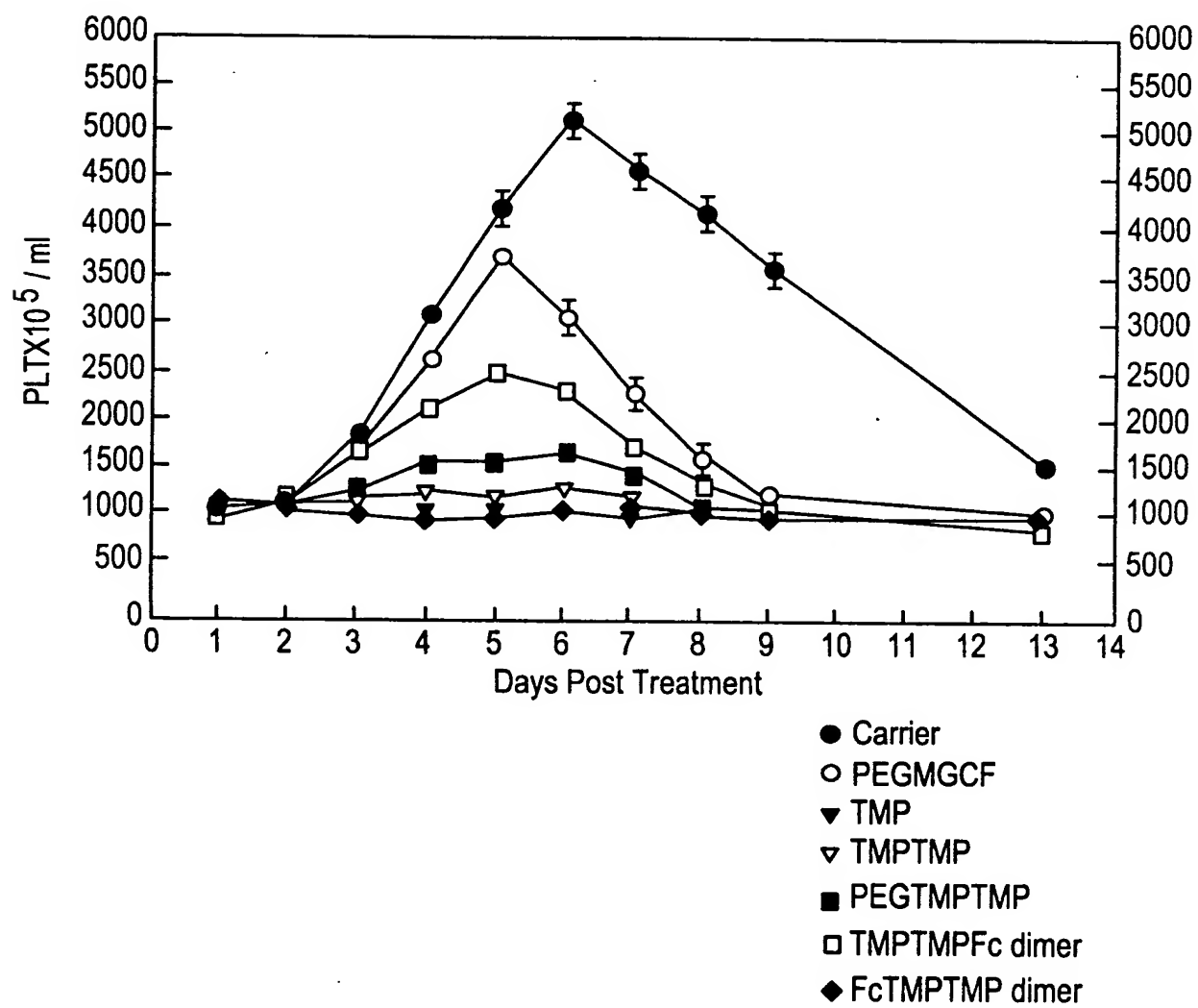


FIG.12

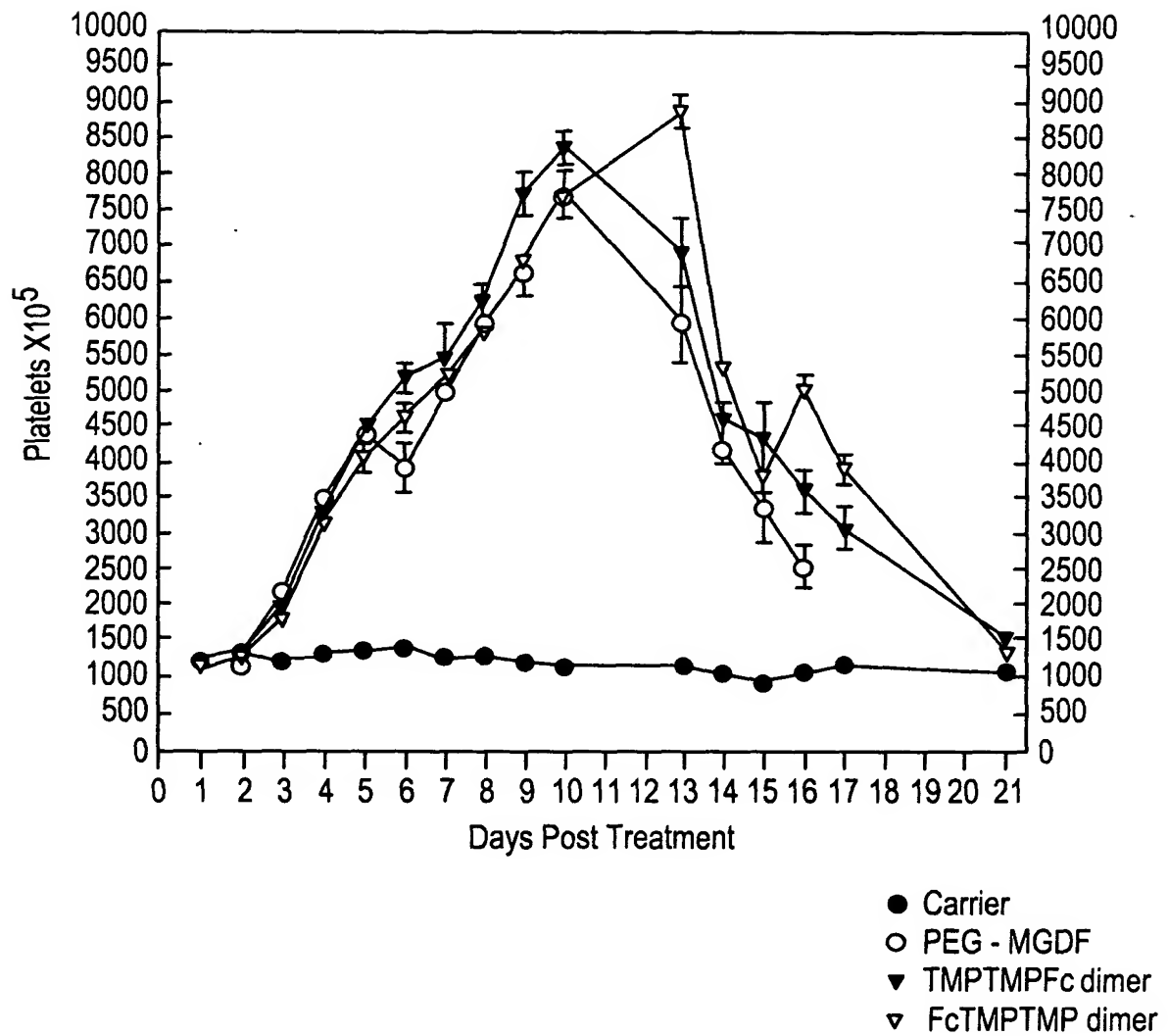




FIG. 14

Xba I

[illegible]

61 ACTTCGGCCCCGCTGACTTGGGTATGTAAGCCACAAGGGGGTGGGGGAGGCGGGGGGGACA 120

[illegible]

181 TCTTCCCCC AAAACCCAAGGACACCCTCATGATCTCCCGACCCCTGAGGTCACATGCG 240  
.....+.....+.....+.....+.....+.....+.....+

241 TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG

TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAACAGCACGTACCGTG

U V H N A R I R F R E E Q I N S T Y R V :

V S V L T V L H Q D W L N G K E Y K C K .

TCCAGAGGTTCGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCG  
 V S N K A L P A P I E K T I S K A K G Q .

TCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGG  
P R E P O V Y T L P P S R D E L T K N O .

TCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCC

501 .....+.....+.....+.....+.....+.....+.....+ 660  
TCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGGCACGACCTGAGGCTGC

[illegible]

721 TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT 780

**BamHI**

GGGACAGAGGCCCATTTATTACCTAGG  
L S P G K \*



# FIG. 16

XbaI  
|  
1 TCTAGATTGTTTAACTAATTAAGGAGGAATAACATATGGACAAAACCTCACACATGTC 60  
AGATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACCTGTTTGTGAGTGTGTACAG  
M D K T H T C P -

61 CACCTTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTCCTCTTCCCCCAAAAC 120  
GTGGAACGGTCTCGTGGACTTGAGGACCCCTGGCAGTCAAAGGAGAAGGGGGTTTTG  
P C P A P E L L G G P S V F L P P P K P -

121 CCAAGGACACCCCTCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA 180  
GGTTCCTGTGGGAGTACTAGAGGGCTGGGGACTCCAGTGTACGCACCACCACCTGCACCT  
K D T L M I S R T P E V T C V V V D V S -

181 GCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG 240  
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGACCTCCACGTATTAC  
H E D P E V K F N W Y V D G V E V H N A -

241 CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA 300  
GGTTCGTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGTCATGGCACACCAAGTCCAGGAGT  
K T K P R E E Q Y N S T Y R V V S V L T -

301 CCGTCCGTCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAG 360  
GGCAGGACGTGGTCTGACCGACTTACCGTTCCCTCATGTTACAGTCCAGAGGTTGTTTC  
V L H Q D W L N G K E Y K C K V S N K A -

361 CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC 420  
GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCTCGTGGGGGCTCTGGTG  
L P A P I E K T I S K A K G Q P R E P Q -

421 AGGTGTACACCCTGCCTCCATCCCGGGATGAGCTGACCAAGAACCAGGTACAGCTGACCT 480  
TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCCGACTGGA  
V Y T L P P S R D E L T K N Q V S L T C -

481 GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540  
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG  
L V K G F Y P S D I A V E W E S N G Q P -

541 CGGAGAACAACACTACAAGACACGCTCCCGTGTGACTCCGACGGCTCCTTCTTCTCTCT 600  
GCCTCTTGTGATGTTCTGGTGGGAGGGCAGGACCTGAGGCTGCCGAGGAAGAAGGAGA  
E N N Y K T T P P V L D S D G S F F L Y -

601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCG 660  
TGTCTGTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC  
S K L T V D K S R W Q Q G N V F S C S V -

661 TGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGGTA 720  
ACTACGTACTCCGAGACGTGTTGGTGTGTCGCTTCTCGGAGAGGGACAGAGGCCCAT  
M H E A L H N H Y T Q K S L S P G K -

721 AAGGTGGAGGTGGTGGCGGAGGTACTTACTCTTGCCACTTCGGCCCACTGACTTGGGTTT 780  
TTCCACCTCCACCACCGCTCCATGAATGAGAACGGTGAAGCCGGGTGACTGAACCCAAA  
G G G G G G G T Y S C H F G P L T W V C -

781 GCAAACCGCAGGGTGGCGGGCGGCGGGCGGTGACCTATTCTGTCAATTTGGCCCCG 840  
CGTTTGGCGTCCACCGCCGCGCGCGCCGACCATGGATAAGGACAGTAAACCGGGCG  
K P Q G G G G G G G G T Y S C H F G P L -

BamHI  
|  
841 TGACCTGGGTATGTAAGCCACAAGGGGGTTAATCTCGAGGATCC 884  
ACTGGACCCATACATTGGTGTCCCCCAATTAGAGCTCCTAGG  
T W V C K P Q G G \*



# FIG. 17A

[AatII sticky end] 5' GCGTAACGTATGCATGGTCTCC-  
 (position #4358 in pAMG21) 3' TGCACGCATTGCATACGTACCAGAGG-

-CCATGCGAGAGTAGGGAACTGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-  
 -GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTCCGAGTCAGCTTTCTGA-

-GGGCCTTTCGTTTTATCTGTTGTTTGTCCGTGAACGCTCTCCTGAGTAGGACAAATCCGC-  
 -CCCGGAAAGCAAAATAGACAACAAACAGCCACTTGCGAGAGGACTCATCTGTTTAGGCG-

-CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCGC-  
 -GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCTCCCACCGCCCGTCTGCGGGCG-

-CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTGCGT-  
 -GTATTTGACGGTCCGTAGTTTAATTTCGTCTCCGGTAGGACTGCCTACCGGAAAAACGCA-

AatII

-TTCTACAACTCTTTTGTTTATTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC-  
 -AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG-

-TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAAATTGCTTTAGAAATACTTTGGCAGC-  
 -AAAATTTTCATACCCGTTAGTTAACGAGGACAATTTTAACGAAATCTTTATGAAACCGTCG-

-GGTTTGTGTTGATTGAGTTTCATTTGCGCATTTGGTTAAATGGAAAGTGACCGTGCGCTTAC-  
 -CCAAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCACTGGCACGCGAATG-

-TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCTTCGCATGCCCACGCTAAAC-  
 -ATGTCGGATTATAAAAACCTTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTTG-

-ATTCTTTTTCTCTTTTGTTAAATCGTTGTTGATTTATTATTTGCTATATTTATTTTTC-  
 -TAAGAAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAAACGATATAAATAAAAAG-

-GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTCATACACGCATGTAAAAATA-  
 -CTATTAATAGTTGATCTCTTCCTTGTTAATTACCATACAAGTATGTGCGTACATTTTTAT-

-AACTATCTATATAGTTGTCTTCTCTGAATGTGCAAACTAAGCATTCCGAAGCCATTAT-  
 -TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTCGTAAGGCTTCGGTAATA-

-TAGCAGTATGAATAGGGAACTAAACCCAGTGATAAGACCTGATGATTTTCGCTTCTTTAA-  
 -ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAATT-

-TTACATTTGGAGATTTTTTATTTACAGCATTTGTTTTCAAATATATTCCAATTAATCGGTG-  
 -AATGTAAACCTCTAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTAAATTAGCCAC-

-AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT-  
 -TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA-

-AATATTGCCTCCATTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG-  
 -TTATAACGGAGGTAAAAAATCCCATTAATAGGTCTTAACCTTATAGTCTAAATTGGTATC-

-AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG-  
 -TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTTACATGGTAAATCAGTATAGTC-

-ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATTCTGT-  
 -TATTCGTAACCTAATTATAGTAATAACGAAGATGTCCGAAATTAATAAATTAATAAGACA-

-AAGTGTCGTCGGCATTTATGCTTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTC-  
 -TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG-

-GCAAGTTTTGCGTGTTATATATCATTAACCGGTAATAGATTGACATTTGATTCTAATAA-  
 -CGTTCAAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAAACTAAGATTATT-

## FIG. 17B

- ATTGGATTTTTGTCACACTATTATATCGCTTGAAATACAATTGTTTAACATAAGTACCTG -  
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC -  
  
- TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTTGATT -  
- ATCCTAGCATGTCCAAATGCGTTCCTTTACCAAACAATATCAGCTAATTAGCTAAACTAA -  
  
- CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA -  
- GATCTAAACAAAATTGATTAATTTCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT -  
  
- GCTCACTAGTGTGCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA -  
- CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT -  
  
- GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA -  
- CTTCTTCTTCTTCTTTTCGGGCTTTCTTCGACTCAACCGACGACGGTGGCGACTCGTTAT -  
  
- ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTTGCTGAAAGGAGG -  
- TGATCGTATTGGGGAACCCCGAGATTTGCCCAGAACTCCCCAAAAACGACTTTCCTCC -  
  
- AACCGCTCTTCACGCTCTTCACGC 3' [SacII sticky end]  
- TTGGCGAGAAGTGCGAGAAGTG 5' (position #5904 in pAMG21)

FIG.18A - 1

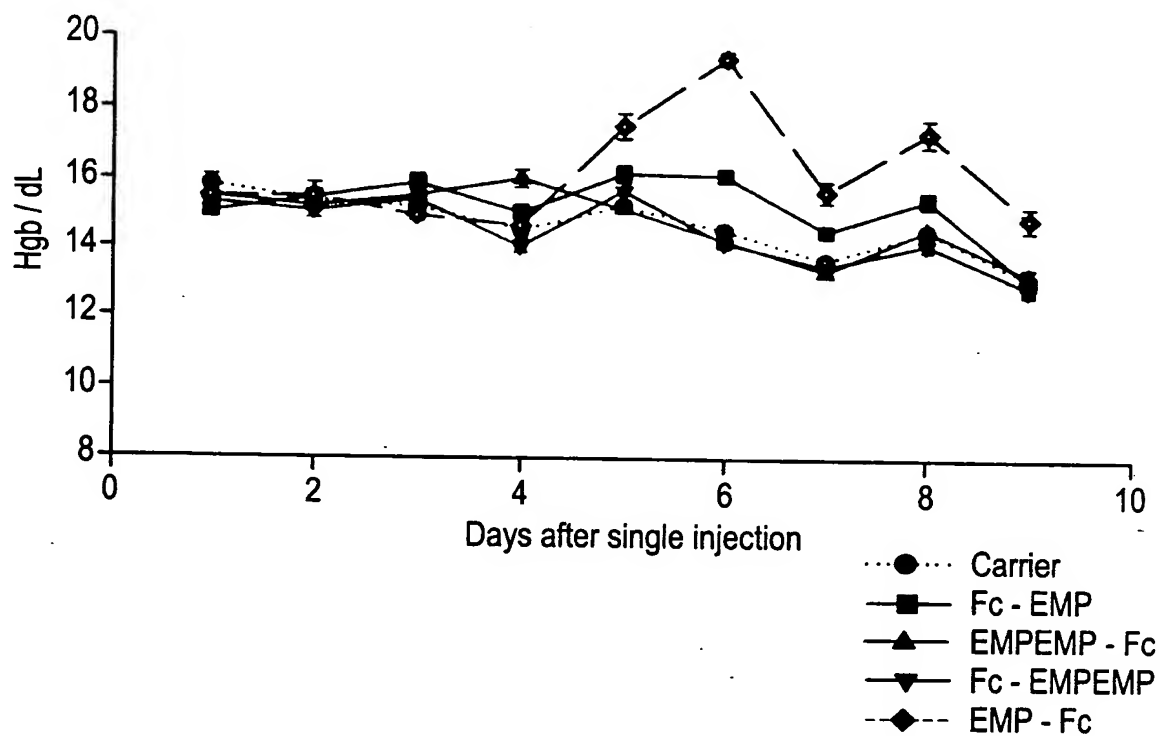


FIG.18A - 2

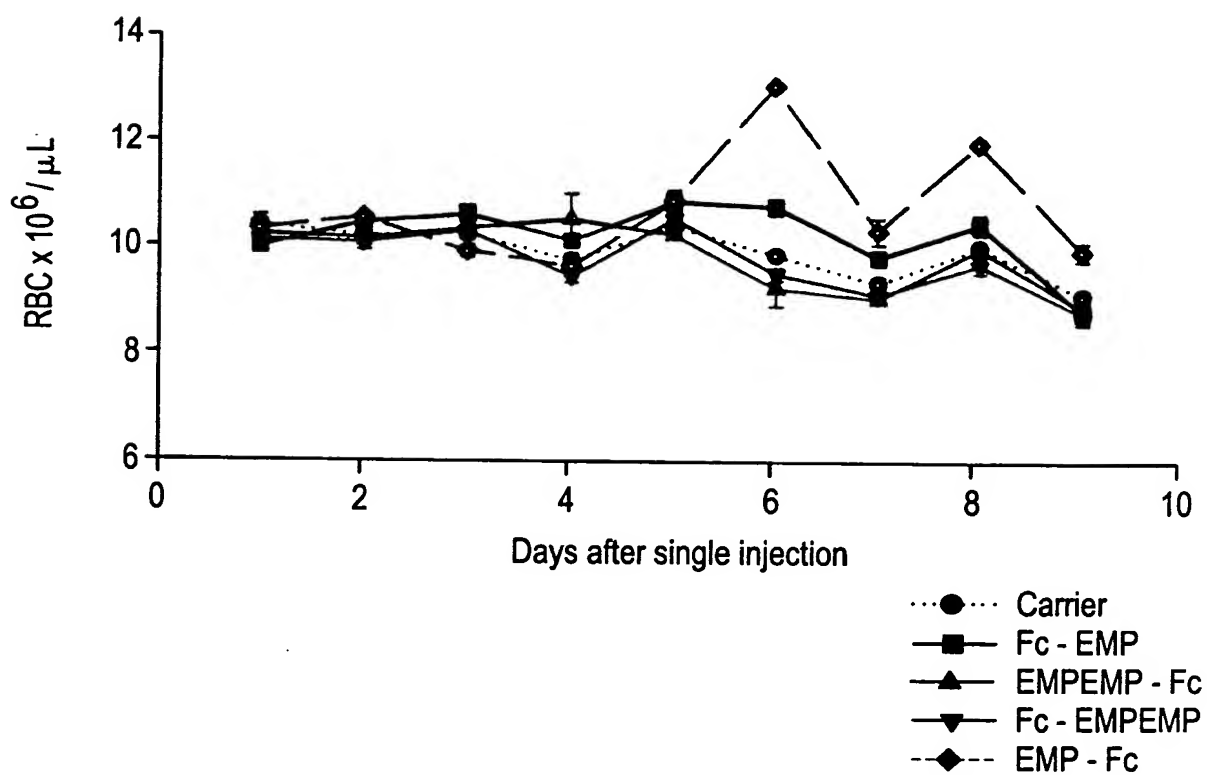


FIG.18A - 3

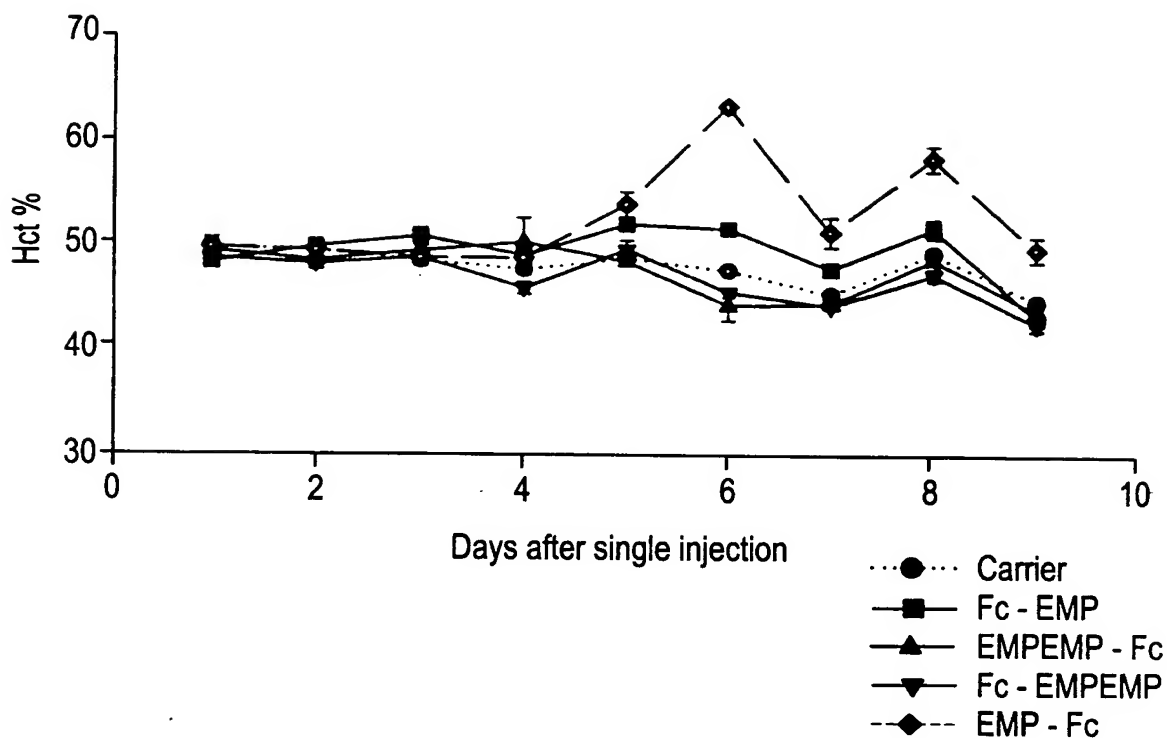


FIG.18B - 1

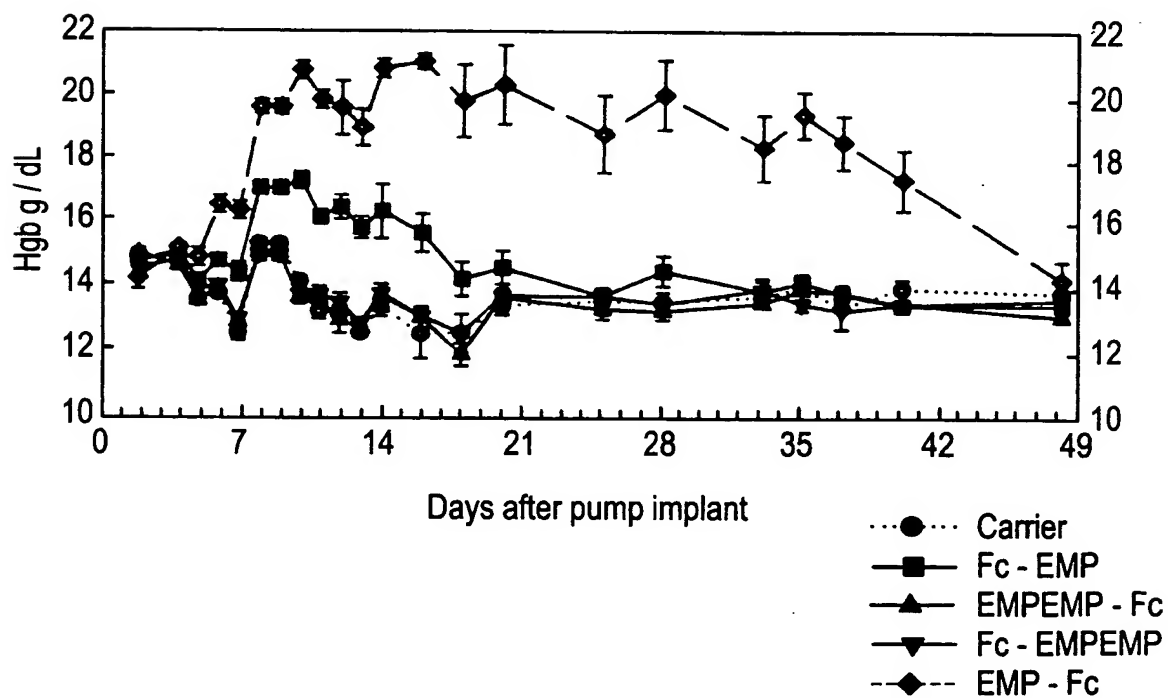


FIG.18B - 2

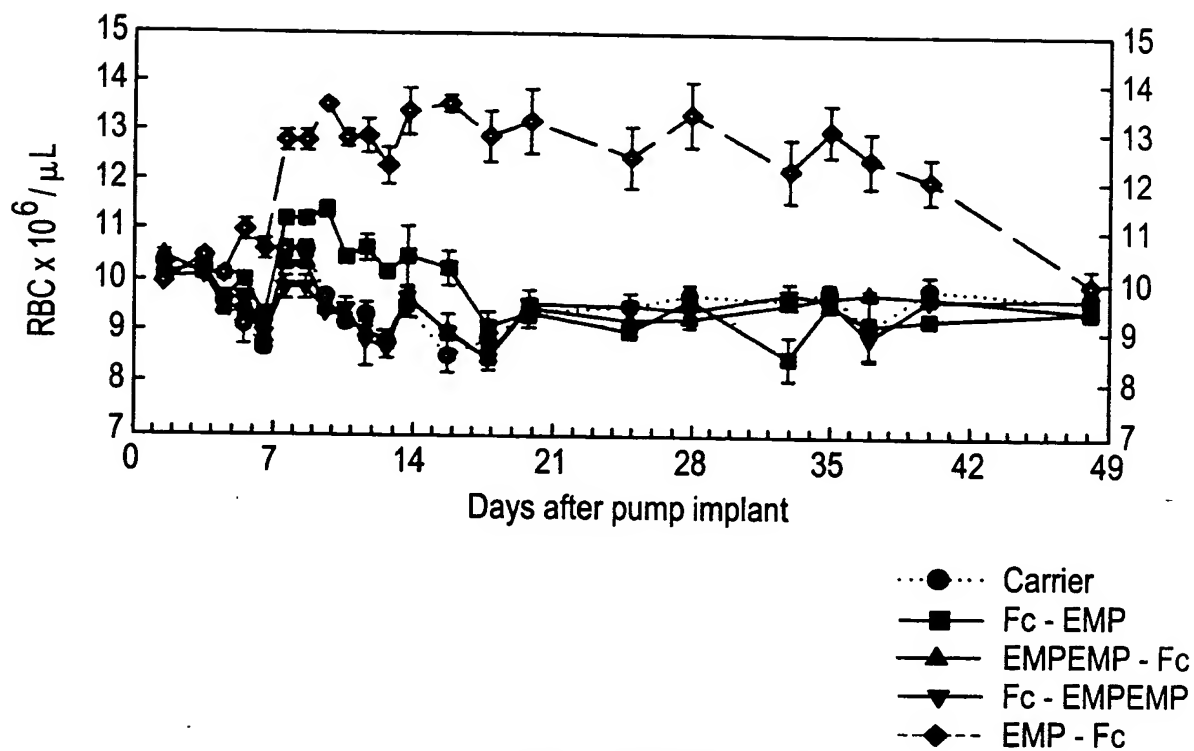
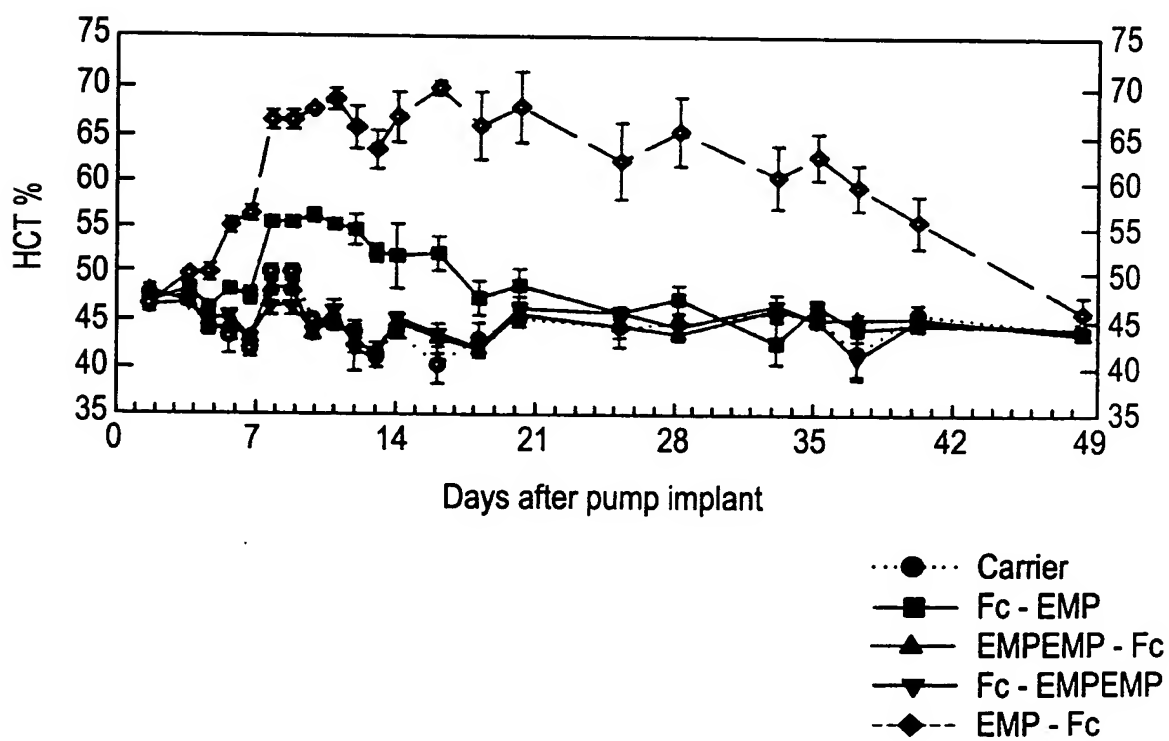


FIG.18B - 3



# FIG. 19A

NdeI

1 CATATGGACAAAACACACATGTCCACCTTGTCAGCTCCGGAACCTCGGGGGGACCG  
-----+-----+-----+-----+-----+-----+-----+ 60  
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTTCGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P .

61 TCAGTCTTCCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG  
-----+-----+-----+-----+-----+-----+ 120  
AGTCAGAAGGAGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E .

121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
-----+-----+-----+-----+-----+-----+ 180  
CAGTGACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y .

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
-----+-----+-----+-----+-----+-----+ 240  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG

a V D G V E V H N A K T K P R E E Q Y N S .

241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
-----+-----+-----+-----+-----+-----+ 300  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E .

301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA  
-----+-----+-----+-----+-----+-----+ 360  
ATGTTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K .

361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
-----+-----+-----+-----+-----+-----+ 420  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L .

421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC  
-----+-----+-----+-----+-----+-----+ 480  
TGGTTCCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A .

481 GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACACTACAAGACCACGCCTCCCGTGCTG  
-----+-----+-----+-----+-----+-----+ 540  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCAGCAG

a V E W E S N G Q P E N N Y K T T P P V L .

541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
-----+-----+-----+-----+-----+-----+ 600  
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q .

## FIG. 19B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  .

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC
-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCACTGAAGGACGGCGTGATG

a      K  S  L  S  L  S  P  G  K  G  G  G  G  G  D  F  L  P  H  Y  .

                                     BamHI
                                     |
721 AAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC
-----+-----+-----+-----+ 757
TTTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG

a      K  N  T  S  L  G  H  R  P  *
```

# FIG. 20A

NdeI  
 |  
 1 CATATGGACTTCCTGCCGCACTACAAAAACACCTCTCTGGGTCACCGTCCGGGTGGAGGC 60  
 -----+-----+-----+-----+-----+-----+-----+  
 GTATACCTGAAGGACGGCGTGATGTTTTGTGGAGAGACCCAGTGGCAGGCCACCTCCG  
 a M D F L P H Y K N T S L G H R P G G G -  
 61 GGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG 120  
 -----+-----+-----+-----+-----+-----+-----+  
 CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCTGTGGACTTGAGGACCCCTGGC  
 a G G D K T H T C P P C P A P E L L G G P -  
 121 TCAGTTTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 180  
 -----+-----+-----+-----+-----+-----+-----+  
 AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
 a S V F L F P P K P K D T L M I S R T P E -  
 181 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 240  
 -----+-----+-----+-----+-----+-----+-----+  
 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
 a V T C V V V D V S H E D P E V K F N W Y -  
 241 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 300  
 -----+-----+-----+-----+-----+-----+-----+  
 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGCG  
 a V D G V E V H N A K T K P R E E Q Y N S -  
 301 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 360  
 -----+-----+-----+-----+-----+-----+-----+  
 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCTCTC  
 a T Y R V V S V L T V L H Q D W L N G K E -  
 361 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA 420  
 -----+-----+-----+-----+-----+-----+-----+  
 ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCTGGGGGTAGCTCTTTTGGTAGAGGTTT  
 a Y K C K V S N K A L P A P I E K T I S K -  
 421 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 480  
 -----+-----+-----+-----+-----+-----+-----+  
 CGGTTTCCCGTCCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
 a A K G Q P R E P Q V Y T L P P S R D E L -  
 481 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 540  
 -----+-----+-----+-----+-----+-----+-----+  
 TGGTTCCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
 a T K N Q V S L T C L V K G F Y P S D I A -  
 541 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG 600  
 -----+-----+-----+-----+-----+-----+-----+  
 CACCTCACCTCTCGTTACCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCAGCAG  
 a V E W E S N G Q P E N N Y K T T P P V L -



## FIG. 20B

```
601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+-----+ 660
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a      D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 720
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG
-----+-----+-----+-----+-----+ 761
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC

a      K S L S L S P G K *
```

# FIG. 21A

NdeI  
|  
CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG  
1 -----+-----+-----+-----+-----+-----+ 60  
GTATACCTGTTTGTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC  
a M D K T H T C P P C P A P E L L G G P -  
TCAGTCTTCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG  
61 -----+-----+-----+-----+-----+ 120  
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
121 -----+-----+-----+-----+-----+ 180  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
181 -----+-----+-----+-----+-----+ 240  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG  
a V D G V E V H N A K T K P R E E Q Y N S -  
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
241 -----+-----+-----+-----+-----+ 300  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC  
a T Y R V V S V L T V L H Q D W L N G K E -  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA  
301 -----+-----+-----+-----+-----+ 360  
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K -  
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
361 -----+-----+-----+-----+-----+ 420  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC  
421 -----+-----+-----+-----+-----+ 480  
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
GTGGAGTGGGAGAGCAATGGGCAGCCGGAACAACACTACAAGACCACGCCTCCCGTGTCTG  
481 -----+-----+-----+-----+-----+ 540  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGGCACGAC  
a V E W E S N G Q P E N N Y K T T P P V L -  
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
541 -----+-----+-----+-----+-----+ 600  
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC  
a D S D G S F F L Y S K L T V D K S R W Q -

## FIG. 21B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGGT
-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA

a      K  S  L  S  L  S  P  G  K  G  G  G  G  G  F  E  W  T  P  G  :

                                     BamHI
                                     |
721 TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
-----+-----+-----+-----+ 763
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC

a      Y  W  Q  P  Y  A  L  P  L  *
```

## FIG. 22A

NdeI  
|  
1 CATATGTTTGAATGGACCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC 60  
-----+-----+-----+-----+-----+-----+-----+  
GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG  
a M F E W T P G Y W Q P Y A L P L G G G -  
GGTGGGGACAAAACCTCACACATGTCCACCTTGCCCAGCACCTGAACCTCTGGGGGGACCG  
61 -----+-----+-----+-----+-----+-----+ 120  
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGC  
a G G D K T H T C P P C P A P E L L G G P -  
TCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAG  
121 -----+-----+-----+-----+-----+-----+ 180  
AGTCAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC -  
181 -----+-----+-----+-----+-----+-----+ 240  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
241 -----+-----+-----+-----+-----+-----+ 300  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGCG  
a V D G V E V H N A K T K P R E E Q Y N S -  
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
301 -----+-----+-----+-----+-----+-----+ 360  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTC  
a T Y R V V S V L T V L H Q D W L N G K E -  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA  
361 -----+-----+-----+-----+-----+-----+ 420  
ATGTTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K -  
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
421 -----+-----+-----+-----+-----+-----+ 480  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
ACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC  
481 -----+-----+-----+-----+-----+-----+ 540  
TGTTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCTCCCGTGCTG  
541 -----+-----+-----+-----+-----+-----+ 600  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCACGAC  
a V E W E S N G Q P E N N Y K T T P P V L -

## FIG. 22B

```
601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAG 660
-----+-----+-----+-----+-----+
CTGAGGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC
a   D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 720
-----+-----+-----+-----+-----+
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC
a   Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC 757
-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a   K S L S L S P G K *
```

## FIG. 23A

NdeI  
|  
1 CATATGGACAAAACCTCACACATGTCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCG 60  
-----+-----+-----+-----+-----+-----+-----+  
GTATACCTGTTTTGAGTGTGTACAGGTGGCACGGGTCTGTGGACTTGAGGACCCCCCTGGC  
a M D K T H T C P P C P A P E L L G G P -  
61 TCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAG 120  
-----+-----+-----+-----+-----+-----+-----+  
AGTCAAAAGGAGAAGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180  
-----+-----+-----+-----+-----+-----+-----+  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240  
-----+-----+-----+-----+-----+-----+-----+  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG  
a V D G V E V H N A K T K P R E E Q Y N S -  
241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300  
-----+-----+-----+-----+-----+-----+-----+  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC  
a T Y R V V S V L T V L H Q D W L N G K E -  
301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360  
-----+-----+-----+-----+-----+-----+-----+  
ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTCTGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K -  
361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420  
-----+-----+-----+-----+-----+-----+-----+  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480  
-----+-----+-----+-----+-----+-----+-----+  
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTG 540  
-----+-----+-----+-----+-----+-----+-----+  
CACCTCACCTCTCGTTACCCGTCTGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGAC  
a V E W E S N G Q P E N N Y K T T P P V L -  
541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600  
-----+-----+-----+-----+-----+-----+-----+  
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCAGTGGCACCTGTTCTCGTCCACCGTC  
a D S D G S F F L Y S K L T V D K S R W Q -

## FIG. 23B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
    .....+.....+.....+.....+.....+.....+.....+.....+ 660
    GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a    Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

    AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGGTGAACCGAACTGTGAC
661 .....+.....+.....+.....+.....+.....+.....+.....+ 720
    TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACCTTGGCTTGACACTG

a    K  S  L  S  L  S  P  G  K  G  G  G  G  G  V  E  P  N  C  D  -

                                     BamHI
                                     |
    ATCCATGTTATGTGGGAATGGGAATGTTTTGAACGTCTGTAACCTCGAGGATCC
721 .....+.....+.....+.....+.....+.....+.....+.....+ 773
    TAGGTACAATACACCCTTACCCTTACAAAACCTGCAGACATTGAGCTCCTAGG

a    I  H  V  M  W  E  W  E  C  F  E  R  L  *
```

# FIG. 24A

NdeI  
|

```

CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGT
1  -----+-----+-----+-----+-----+-----+-----+ 60
GTATACCAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACCTTGCA

a      M V E P N C D I H V M W E W E C F E R -

CTGGGTGGTGGTGGTGGTGACAAACTCACACATGTCCACCGTGCCAGCACCTGAACTC
61  -----+-----+-----+-----+-----+-----+-----+ 120
GACCCACCACCACCACCCTGTTTTGAGTGTGTACAGGTGGCAGGGTCGTGGACTTGAG

a      L G G G G G D K T H T C P P C P A P E L -

CTGGGGGGACCGTCAGTTTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCC
121  -----+-----+-----+-----+-----+-----+-----+ 180
GACCCCCCTGGCAGTCAAAGGAGAAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGG

a      L G G P S V F L F P P K P K D T L M I S -

CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG
181  -----+-----+-----+-----+-----+-----+-----+ 240
GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC

a      R T P E V T C V V V D V S H E D P E V K -

TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG
241  -----+-----+-----+-----+-----+-----+-----+ 300
AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC

a      F N W Y V D G V E V H N A K T K P R E E -

CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGGCTG
301  -----+-----+-----+-----+-----+-----+-----+ 360
GTCATGTTGTCTGTCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTCTGACCGAC

a      Q Y N S T Y R V V S V L T V L H Q D W L -

AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAA
361  -----+-----+-----+-----+-----+-----+-----+ 420
TTACCGTTCCTCATGTTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT

a      N G K E Y K C K V S N K A L P A P I E K -

ACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
421  -----+-----+-----+-----+-----+-----+-----+ 480
TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG

a      T I S K A K G Q P R E P Q V Y T L P P S -

CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCC
481  -----+-----+-----+-----+-----+-----+-----+ 540
GCCCTACTCGACTGGTTCCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG

a      R D E L T K N Q V S L T C L V K G F Y P -

AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATAAGACCACG
541  -----+-----+-----+-----+-----+-----+-----+ 600
TCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGC

a      S D I A V E W E S N G Q P E N N Y K T T -

```



## FIG. 24B

```

601 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAG 660
    -----+-----+-----+-----+-----+-----+
    GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC
a      P P V L D S D G S F F L Y S K L T V D K .

661 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC 720
    -----+-----+-----+-----+-----+-----+
    TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG
a      S R W Q Q G N V F S C S V M H E A L H N .

                                     BamHI
                                     |
721 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC 773
    -----+-----+-----+-----+-----+-----+
    GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG
a      H Y T Q K S L S L S P G K *
```

# FIG. 25A

NdeI  
|  
1 CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCG 60  
-----+-----+-----+-----+-----+  
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCTGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

61 TCAGTCTTCTCTTCCCCCAAACCCAAGGACACCTCATGATCTCCCGGACCCCTGAG 120  
-----+-----+-----+-----+-----+  
AGTCAGAAGGAGAAGGGGGTGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180  
-----+-----+-----+-----+-----+  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240  
-----+-----+-----+-----+-----+  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCTG

a V D G V E V H N A K T K P R E E Q Y N S -

241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300  
-----+-----+-----+-----+-----+  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA 360  
-----+-----+-----+-----+-----+  
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCTGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420  
-----+-----+-----+-----+-----+  
CGGTTTCCCGTCCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480  
-----+-----+-----+-----+-----+  
TGTTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGTCTG 540  
-----+-----+-----+-----+-----+  
CACCTCACCCCTCTCGTTACCCGTCGGCCTCTTGTGTGATGTTCTGGTGCGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600  
-----+-----+-----+-----+-----+  
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCAGGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

## FIG. 25B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q   G   N   V   F   S   C   S   V   M   H   E   A   L   H   N   H   Y   T   Q   -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCACTGGGGT
-----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA

A   K   S   L   S   L   S   P   G   K   G   G   G   G   G   C   T   T   H   W   G   -

      BamHI
      |
721 TTCACCCTGTGCTAATGGATCCCTCGAG
-----+-----+-----+-----+ 748
AAGTGGGACACGATTACCTAGGGAGCTC

a   F   T   L   C   *
```

# FIG. 26A

NdeI  
|  
CATATGTGCACCACCCACTGGGGTTTCACCCTGTGCGGTGGAGGCGGTGGGGACAAAGGT  
1 .....+.....+.....+.....+.....+.....+.....+ 60  
GTATACACGTGGTGGGTGACCCCAAAGTGGGACACGCCACCTCCGCCACCCCTGTTTCCA

a M C T T H W G F T L C G G G G G D K G -

61 GGAGGCGGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGG  
.....+.....+.....+.....+.....+.....+.....+ 120  
CCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCTGTGGACTTGAGGACCCC

a G G G G D K T H T C P P C P A P E L L G -

121 GGACCGTCAGTTTTCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACC  
.....+.....+.....+.....+.....+.....+.....+ 180  
CCTGGCAGTCAAAGGAGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGG

a G P S V F L F P P K P K D T L M I S R T -

181 CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC  
.....+.....+.....+.....+.....+.....+.....+ 240  
GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG

a P E V T C V V V D V S H E D P E V K F N -

241 TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC  
.....+.....+.....+.....+.....+.....+.....+ 300  
ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG

a W Y V D G V E V H N A K T K P R E E Q Y -

301 AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC  
.....+.....+.....+.....+.....+.....+.....+ 360  
TTGTCTGTGCATGGCACACCAAGTCGCAGGAGTGGCAGGACGTGGTCTTGACCGACTTACCG

a N S T Y R V V S V L T V L H Q D W L N G -

361 AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATC  
.....+.....+.....+.....+.....+.....+.....+ 420  
TTCCTCATGTTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG

a K E Y K C K V S N K A L P A P I E K T I -

421 TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT  
.....+.....+.....+.....+.....+.....+.....+ 480  
AGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTA

a S K A K G Q P R E P Q V Y T L P P S R D -

481 GAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC  
.....+.....+.....+.....+.....+.....+.....+ 540  
CTCGACTGGTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTG

a E L T K N Q V S L T C L V K G F Y P S D -

541 ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACATAAGACCACGCCTCCC  
.....+.....+.....+.....+.....+.....+.....+ 600  
TAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGG

a I A V E W E S N G Q P E N N Y K T T P P -

## FIG. 26B

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601 GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG
-----+-----+-----+-----+-----+-----+-----+ 660
CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCC
a   V L D S D G S F F L Y S K L T V D K S R .

661 TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
-----+-----+-----+-----+-----+-----+ 72
ACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG
a   W Q Q G N V F S C S V M H E A L H N H Y .

                                     BamHI
                                     |
721 ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
-----+-----+-----+-----+-----+ 763
TGCCTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a   T Q K S L S L S P G K *
```